

Application No. 09/934,455

Docket No.: MBI-0025

Listing of Claims

Claim 1. (Currently amended) A transgenic plant comprising a recombinant polynucleotide having a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising ~~an amino acid sequence selected from those of SEQ ID NOs. 2N where N=1-258~~ SEQ ID NO: 6, or a complementary nucleotide sequence thereof;
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) ~~one of SEQ ID NOs. 2N-1 where N=1-258~~ SEQ ID NO: 5, or a complementary nucleotide sequence thereof;
- (d) a nucleotide sequence comprising one or more silent substitutions in a nucleotide sequence of (c);
- (e) a nucleotide sequence that hybridizes under stringent conditions of 0.2 x SSC, 0.1% SDS at 65° C to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any of (a)-(g);
- (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6;
- (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6; or
- (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6;

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- (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6;
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the entire length of ~~a polypeptide of one of SEQ ID Nos.: 2N where N=1-258~~ SEQ ID NO: 6,
- wherein the plant possesses an altered trait as compared to a wild type or reference plant, or the plant exhibits an altered phenotype as compared to a wild type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild-type plant.

Claim 2. (Original) The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to said recombinant nucleotide.

Claim 3. (Original) The transgenic plant of claim 1, wherein the plant is selected from the following group: soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,

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grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, *Arabidopsis*, spinach, squash, sweet corn, tobacco, tomato, watermelon, mint and other labiates, rosaceous fruits, and vegetable brassicas.

Claim 4. (Currently amended) An isolated or recombinant polynucleotide having a nucleotide sequence selected from the ~~following group consisting of:~~

- (a) a nucleotide sequence encoding a polypeptide comprising ~~a sequence selected from those of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6, or a complementary nucleotide sequence thereof;
- (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a);
- (c) ~~one of SEQ ID NOs. 2N-1 where N=1-258~~ SEQ ID NO: 5, or a complementary nucleotide sequence thereof;
- (d) a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c);
- (e) a nucleotide sequence that hybridizes under stringent conditions of 0.2 x SSC, 0.1% SDS at 65° C to a nucleotide sequence of one or more of: (a), (b), (c), or (d);
- (f) a nucleotide sequence comprising at least 15 consecutive nucleotides outside of a conserved domain of any of (a)-(e);
- (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), which subsequence or fragment encodes a polypeptide that modifies one or more of a plant's traits;
- (h) a nucleotide sequence having at least 31% sequence identity to a nucleotide sequence of any of (a)-(g);
- (i) a nucleotide sequence having at least 60% sequence identity to a nucleotide sequence of any of (a)-(g);
- (j) a nucleotide sequence having at least 95% sequence identity to a nucleotide sequence of any of (a)-(g);
- (k) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6;
- (l) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos. 2N where N=1-258~~ SEQ ID NO: 6; or

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- (m) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (n) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity outside of a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (o) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least 86% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (p) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 90% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (q) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 95% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6; and
- (r) a nucleotide sequence encoding a polypeptide having an amino acid domain with at least about 98% sequence identity to a conserved domain of a polypeptide having an amino acid sequence of ~~one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (s) a nucleotide sequence encoding a polypeptide having at least 31% sequence identity over the entire length of a ~~polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (t) a nucleotide sequence encoding a polypeptide having at least 60% sequence identity over the entire length of a ~~polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6;
- (u) a nucleotide sequence encoding a polypeptide having at least 75% sequence identity over the entire length of a ~~polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6; and
- (v) a nucleotide sequence encoding a polypeptide having at least 95% sequence identity over the entire length of a ~~polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N~~ where ~~N=1-258~~ SEQ ID NO: 6.

Claim 5. (Original) The isolated or recombinant polynucleotide of claim 4, further comprising a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide nucleotide.

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Claim 6. (Original) An isolated or recombinant polypeptide comprising a subsequence of at least about 15 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4.

Claim 7. (Original) A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress the polypeptide, thereby producing a modified plant, and selecting for a modified trait.

Claim 8. (Currently amended) The transgenic plant of claim 1, wherein the trait is selected from the group: consisting of enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; ~~enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone;~~ enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; and enhanced tolerance to pest infestation; ~~decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.~~

Claim 9. (Currently amended) The transgenic plant of claim 1, wherein the trait is an alteration in the level of ~~one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenolipids, glucosinolates, and terpenoids.~~

Claim 10. (Canceled) The transgenic plant of claim 1, wherein the trait is an alteration in one or more physical characteristics selected from the group: number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of seed coat.

Claim 11. (Currently amended) The transgenic plant of claim 1, wherein the trait is an alteration in a plant growth characteristic selected from the group: consisting of growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; and more tolerance to growth under nitrogen-limiting conditions; ~~biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.~~

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Claim 12. (Canceled) The transgenic plant of claim 1, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.

Claim 13. (Currently amended) The method of claim 7, wherein the trait is selected from the group consisting of enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; ~~enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone;~~ enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; and enhanced tolerance to pest infestation; ~~decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.~~

Claim 14. (Currently amended) The method of claim 7, wherein the trait is an alteration in the level of ~~one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenylipids, glucosinolates, and terpenoids.~~

Claim 15. (Canceled) The method of claim 7, wherein the trait is an alteration in one or more physical characteristics selected from the group: consisting of number of trichomes; fruit and seed size and number; yield of stems; yield of leaves; yield of roots; stability of seeds during storage; susceptibility of the seed to shattering; root hair length; root hair quantity; internode distances; and the quality of seed coat.

Claim 16. (Currently amended) The method of claim 7, wherein the trait is an alteration in a plant growth characteristic selected from the group: consisting of growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; and more tolerance to growth under nitrogen-limiting conditions; ~~biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.~~

Claim 17. (Canceled) The method of claim 7, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.

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Claim 18. (Original) A plant produced by the method of claim 13.

Claim 19. (Original) A plant produced by the method of claim 14.

Claim 20. (Original) A plant produced by the method of claim 15.

Claim 21. (Original) A plant produced by the method of claim 16.

Claim 22. (Original) A plant produced by the method of claim 17.

Claim 23. (Original) A method of using the isolated or recombinant polynucleotide of claim 4 for producing a plant having a modified trait, the method comprising selecting a polynucleotide that when expressed produces an antisense nucleic acid, inserting the polynucleotide into an expression vector, introducing the vector into a plant or a cell of a plant to express the antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trait.

Claim 24. (Currently amended) The method of claim 23, wherein the trait is selected from the group consisting of enhanced tolerance to freezing; enhanced tolerance to chilling; enhanced tolerance to heat; enhanced tolerance to drought; ~~enhanced tolerance to water saturation; enhanced tolerance to radiation; enhanced tolerance to ozone;~~ enhanced tolerance to microbial disease; enhanced tolerance to fungal disease; enhanced tolerance to viral disease; and enhanced tolerance to pest infestation; ~~decreased herbicide sensitivity; enhanced tolerance to heavy metals; enhanced ability to take up heavy metals; and enhanced growth under poor photoconditions.~~

Claim 25. (Currently amended) The method of claim 23, wherein the trait is an alteration in the level of ~~one or more of the compounds selected from the group: taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, anti-oxidants, amino acids, lignins, cellulose, tannins, prenyllipids, glucosinolates, and terpenoids.~~

Claim 26. (Canceled) The method of claim 23, wherein the trait is an alteration in one or more physical characteristics selected from the group consisting of: the number of trichomes, fruit and seed size and number, yield of stems, leaves, or roots, stability of seeds during storage, susceptibility of the seed to shattering, root hair length and quantity, internode distances, or the quality of seed coat.

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Claim 27. (Currently amended) The method of claim 23, wherein the trait is an alteration in a plant growth characteristic selected from the group: consisting of growth rate; germination rate of seeds; vigor of plants; vigor of seedlings; leaf senescence; flower senescence; male sterility; apomixis; flowering time; flower abscission; rate of nitrogen uptake; and more tolerance to growth under nitrogen-limiting conditions; biomass; transpiration characteristics; apical dominance; branching pattern; number of organs; organ identity; organ shape; and organ size.

Claim 28. (Canceled) The method of claim 23, wherein the trait is an alteration in one or more characteristics selected from the group: protein production; oil production; seed protein production; seed oil production; insoluble sugar level; soluble sugar level; and starch composition.

Claim 29. (Original) A plant produced by the method of claim 24.

Claim 30. (Original) A plant produced by the method of claim 25.

Claim 31. (Original) A plant produced by the method of claim 26.

Claim 32. (Original) A plant produced by the method of claim 27.

Claim 33. (Original) A plant produced by the method of claim 28.

Claim 34. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 10 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are outside of a conserved domain.

Claim 35. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 20 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are outside of a conserved domain.

Claim 36. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are outside of a conserved domain.



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Claim 37. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 10 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are within a conserved domain.

Claim 38. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 20 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are within a conserved domain.

Claim 39. (Withdrawn) An isolated or recombinant polypeptide comprising a subsequence of at least about 30 contiguous amino acids encoded by the recombinant or isolated polynucleotide of claim 4, wherein the contiguous amino acids are within a conserved domain.

Claim 40. (Withdrawn) An isolated or recombinant polypeptide having at least 31% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-258, or the length of the polypeptide itself.

Claim 41. (Withdrawn) An isolated or recombinant polypeptide having at least 60% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-258, or the length of the polypeptide itself.

Claim 42. (Withdrawn) An isolated or recombinant polypeptide having at least 75% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-258, or the length of the polypeptide itself.

Claim 43. (Withdrawn) An isolated or recombinant polypeptide having at least 95% sequence identity over the entire length of a polypeptide having an amino acid sequence of one of SEQ ID Nos.: 2N where N=1-258, or the length of the polypeptide itself.

Claim 44. (Currently amended) An isolated or recombinant polynucleotide having the sequence ~~one of SEQ ID Nos.: 2N-1 where N=1-258~~ SEQ ID NO: 5, or a complementary nucleotide sequence thereof.

Claims 45-47 (Canceled)

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Claim 48. (Withdrawn) A computer readable medium having stored sequence information comprising the polynucleotide sequence of claim 44.

Claim 49. (Withdrawn) The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 1-37.

Claim 50. (Withdrawn) The computer readable medium of claim 48, having stored sequence information comprising the sequence of one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

Claim 51. (Withdrawn) The computer readable medium of claim 48, having stored sequence information comprising the polynucleotide sequence of one of SEQ ID Nos.: 345, 346, 365, 366, 447, 448, 469, 470, 477, 478, 505, 506, 507, 508, 509, 510, 511, 512, 513, or 514.

Claim 52. (Withdrawn) A method of identifying a homolog sequence from a database comprising a plurality of known plant sequences, the method comprising: inputting sequence information selected from one or more of SEQ ID Nos. 1-516; and querying the database to identify a homolog sequence.

Claim 53. (Withdrawn) The method of claim 52, wherein the database being queried comprises a database of known genomic, cDNA, EST, or protein sequences.

Claim 54. (Withdrawn) The method of claim 52, wherein inputting sequence information comprises copying the sequence information from a CD.

Claim 55. (Withdrawn) The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 1-37.

Claim 56. (Withdrawn) The method of claim 52, wherein the sequence data comprises one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

Claim 57. (Withdrawn) The method of claim 52, wherein the sequence data comprises of SEQ ID Nos.: 345, 346, 365, 366, 447, 448, 469, 470, 477, 478, 505, 506, 507, 508, 509, 510, 511, 512, 513, or 514.

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Claim 58. (Withdrawn) The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 1-37.

Claim 59. (Withdrawn) The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acids region one of SEQ ID Nos.: 53, 54, 79, 80, 81, 82, 107, 108, 125, 126, 153, 154, 167, 168, 203, 204, 223, 224, 289, 290, 285, 286, 287, or 288.

Claim 60. (Withdrawn) The method of claim 52, wherein the sequence data comprises a 20 nucleotide region or 6 amino acid region of one of SEQ ID Nos.: 345, 346, 365, 366, 447, 448, 469, 470, 477, 478, 505, 506, 507, 508, 509, 510, 511, 512, 513, or 514.

Claim 61. (Withdrawn) A homolog identified by the method of claim 52.

Claim 62. (Withdrawn) The homolog of claim 61, identified by the method of claim 53.

Claim 63. (Withdrawn) The homolog of claim 61, identified by the method of claim 54.

Claim 64. (Withdrawn) The homolog of claim 61, identified by the method of claim 55.

Claim 65. (Withdrawn) The homolog of claim 61, identified by the method of claim 55.

Claim 66. (Withdrawn) The homolog of claim 61, identified by the method of claim 56.

Claim 67. (Withdrawn) The homolog of claim 61, identified by the method of claim 57.

Claim 68. (Withdrawn) The homolog of claim 61, identified by the method of claim 58.

Claim 69. (Withdrawn) The homolog of claim 61, identified by the method of claim 59.

Claim 70. (Withdrawn) The homolog of claim 61, identified by the method of claim 60.